In the claims:

1.   (Currently Amended)   A method of identifying heterogeneous features in an image of an array of features, said method comprising:

      (a)   determining a toggle parameter for said array of features; and

      (b)   identifying features as heterogeneous that:

          (i)   have a signal intensity that is equal to or less than the toggle parameter and has a first intra-feature noise metric **that exceeds** a first intra-feature noise metric limit; or

          (ii)   have a signal intensity that is greater than the toggle parameter and has a second intra-feature noise metric that exceeds the second intra-feature noise metric limit;

whereby heterogeneous features in said image are identified.

2.   (Currently Amended)   The method according to Claim 1, wherein said first intra-feature noise metric is intra-feature standard deviation **and** said second intra-feature noise **metric** ~~value~~ is intra-feature coefficient of variation.

3.   (Original)   The method according to Claim 1, wherein said image is an image of a biopolymeric array.

4.   (Original)   The method according to Claim 1, wherein said toggle parameter is a toggle point.

5.   (Currently Amended)   The method according to Claim **4** 1, wherein said toggle point is determined from statistics obtained from low signal features of said array.

6.   (Original)   The method according to Claim 5, wherein said toggle point is the intersection of a toggle line and a high signal coefficient of variation limit.

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7.   (Currently Amended)   A method of identifying heterogeneous features in an image of a nucleic acid array, said method comprising:

    (a)   determining a toggle point for said image; and

    (b)   identifying features as heterogeneous that:

        (i)   have a signal intensity that is less than or equal to said toggle point and have an intra-feature standard deviation that exceeds a standard deviation limit; ~~and~~ or

        (ii)   have a signal intensity that exceeds said toggle point and have an intra-feature coefficient of variation that exceeds a coefficient of variation limit;

    whereby heterogeneous features in said image of said nucleic acid array are identified.

8.   (Original)   The method according to Claim 7, wherein said toggle point is determined from statistics obtained from low signal features.

9.   (Original)   The method according to Claim 7, wherein said toggle point determination comprises deriving a toggle line from said low signal feature statistics.

10.   (Original)   The method according to Claim 9, wherein said toggle point is the intersection of said toggle line and a high signal coefficient of variation limit.

11.   (Currently Amended)   A method of identifying heterogeneous features in an image of a nucleic acid array, said method comprising:

    (a)   determining a toggle point for said array of features from statistics obtained from low signal features of said image; and

    (b)   identifying features as heterogeneous that:

        (i)   have a signal intensity that is less than or equal to said toggle point and have an intra-feature standard deviation that exceeds a standard deviation limit; ~~and~~ or

        (ii)   have a signal intensity that exceeds said toggle point and have an intra-feature coefficient of variation that exceeds a coefficient of variation limit;

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whereby heterogeneous features in said image of said nucleic acid array are identified.

12.   (Original)   The method according to Claim 11, wherein said toggle point determination comprises deriving a toggle line from said low signal feature statistics.

13.   (Original)   The method according to Claim 12, wherein said toggle point is the intersection of said toggle line and a high signal coefficient of variation limit.

14.   (Currently Amended)   A computer readable storage medium on which is recorded an algorithm for identifying heterogeneous image features in an image of an array, wherein said algorithm performs the steps of:
        (a)   determining a toggle point for said image; and
        (b)   identifying features as heterogeneous that:
            (i)   have a signal intensity that is less than or equal to said toggle point and have an intra-feature standard deviation that exceeds a standard deviation limit; and or
            (ii)   have a signal intensity that exceeds said toggle point and have an intra-feature coefficient of variation that exceeds a coefficient of variation limit.

15.   (Original)   The computer readable storage medium according to Claim 14, wherein said image is an image of a biopolymeric array.

16.   (Original)   The computer readable storage medium according to Claim 15, wherein said biopolymeric array is a nucleic acid array.

17.   (Original)   The computer readable storage medium according to Claim 14, wherein said toggle point is determined from statistics obtained from low signal features.

18.   (Original)   The computer readable storage medium according to Claim 17, wherein said toggle point determination comprises deriving a toggle line from said low signal feature statistics.

19.   (Original)   The computer readable storage medium according to Claim 18, wherein said toggle point is the intersection of said toggle line and a high signal coefficient of variation limit.

20.   (Original)   A method of detecting the presence of an analyte in a sample, said method comprising:

    (a)   contacting (i) a biopolymeric array having a polymeric ligand that specifically binds to said analyte, with (ii) a sample suspected of comprising said analyte under conditions sufficient for binding of said analyte to a biopolymeric ligand on said array to occur;

    (b)   detecting the presence of binding complexes on the surface of the said array to obtain assay data in the form of an array image;

    (c)   processing said array image to identify heterogenous features according to the method of Claim 1;

    (d)   employing said processed array image to detect the presence of said analyte in said sample.

21.   (Original)   The method according to Claim 20, wherein said method further comprises a data transmission step in which a result from a reading of the array is transmitted from a first location to a second location.

22.   (Original)   A method according to Claim 21 wherein said second location is a remote location.

23.   (Original)   A method comprising receiving data representing a result of a reading obtained by the method of Claim 20.